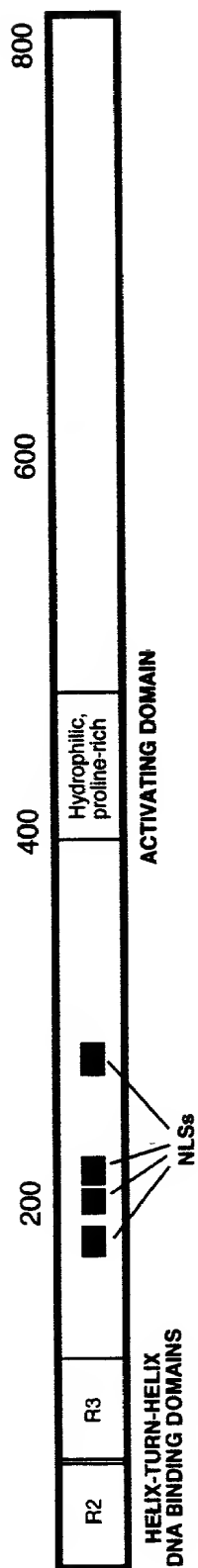


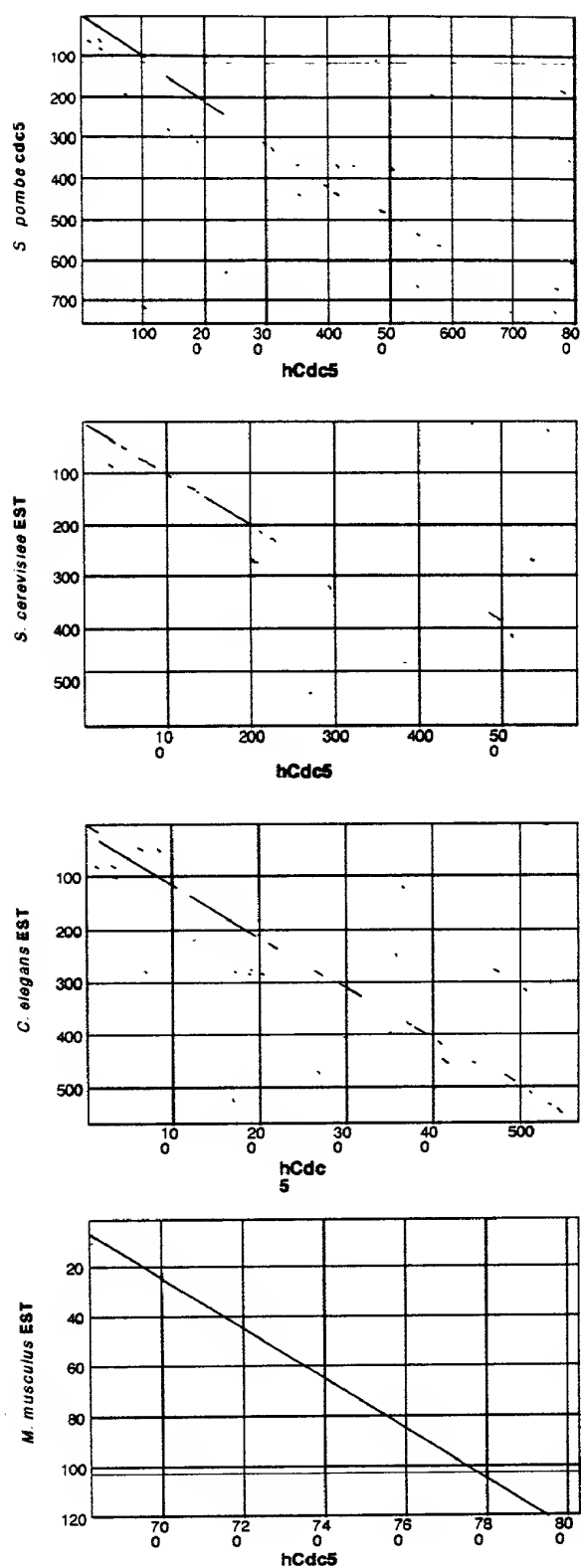
MPRIMIKGGVWRNTEDEILKAAVMKYGKNQWSRIASLLHRKSAKQCKARW 50  
 YEWLDPSIKKTEWSREEEEKLLHLAKLMPTQWRTIAPIIGRTAAQCLEHY 100  
 EFLLDKAAQRDNEEETTDDPRKLKPGEIDPNPETKPARPDPIDMDEDELE 150  
 MLSEARARLANTQGKKAKRKAREKQLEEARRLAALQKRRELRAAGIEIQK 200  
 KRKRKRGVDYNAEIPFEKKPALGFYDTSEENYQALDADFRKL RQQDL DGE 250  
 LRSEKEGRDRKKDKOHLKRKKESDLPSAILQTSGVSEFTKKRSKLVLPAP 300  
 QISDAELQEVVKVGQASEIARQTAEESGITNSASSTLLSEYNVTNNSVAL 350  
 RTPRTPASQDRILQEAQNLMA LTNVDTPLKGG LNTPLHESDFSGVTPQRO 400  
 VVQTPNTVLSTPFRTPSNGAEG LTPRSGTTPKPVINSTPGRTPLRDKLNI 450  
 NPEDGMADYSDPSYVKOMERESREHLRLGLLGLPAPKNDFEIVLPENAEK 500  
 ELEEREIDDTYIEDAADVDARKQAIRDAERVKEMKRMHKAVQKDLPRPSE 550  
 VNETILRPLNVEPPLTDLQKSEELIKKEMITMLHYDLLHHPYEPGNNKKG 600  
 KTVGFGTNNSEHITYLEHNPYEKFSKEELKKAQDVLVQEMEVVKQGMSHG 650  
 ELSSEAYNQVWEECYSQLYLPGQSR YTRANLASKKDRIESLEKRLEINR 700  
 GHMTTEAKRAAKMEKKMKILLGGYQSRAMGLMKQLNDLWDQIEQAHLER 750  
 TFEELKKHEDSAIPRRLECLKEDVQRQQEREKELQHRYADLLLEKETLKS 800

KF\*

Fig. 1A



**Fig. 1B**



**Fig. 2A**

hCdc5	IKGGVWRNTEDEILKAAVMKYGKNQWSRIASLLHRKSAKQCKARWYEWLDP	(6-56)
<i>Spombe</i> cdc5	LIKGGAWKNTTEDEILKAAVSKY GKNQWARISSLLVRKTPKQCKARWYEWIDP	(5-55)
b-Myb	V/K-GPWTKEEDQKVIELVKKYGTQWTLIAKHLKGRLGKQCRERWNNHHLNIP	(88-137)
a-Myb	IK-GPWTKEEDQKVIELVQKYGPKRWSLIAKHLKGRIGKQCRERWNNHHLNIP	(87-136)
c-Myb	IK-GPWTKEEDQKVIELVQKYGPKRWSVIAKHLKGRIGKQCRERWNNHHLNIP	(92-141)

Fig. 2B

hCdc5  
*S. pombe* cdc5  
b-Myb  
a-Myb

PLKGGGLNTPLHESDFSGVTPQRQVVQTPNTVLSTPFRTPSNGAEGLTPRSGLTPKPVINSTP (378-439)  
SVTIEVRNQLMNRQSSLLGQESIPQGGTGYTGVT-PSHAANGS---ALAAP--Q--ATP (380-434)  
PVK-TL--PFSPSQFLNFWNKQDTLEESPLSTPVCQKVVVTTPLHRDKTPLHQQKHAFF (445-503)  
ILRKKRKMVRVGHSPGSEL-RDGSUNDGGNMALKTPLKTPFSPSQFFNTCPGNEQLNIENPSF (446-508)

hCdc5  
*S. pombe* cdc5  
b-Myb  
a-Myb

GRTPLRDKLNPREDGMADYSDPSYVKQMERESREHLRLGLLGLPAPKNDFEIVLPENAEK (440-500)  
FRTPR-DTFSINAAAERAGR-LASE-REN-KIRLKALRELLAKLPKPKNDYEL-ME-P-R- (435-487)  
VTPDQKYSMDNTRHTP-TPFKNAKYGPLKPLPQTPHLEEDLKEVLRSEAGIELIIEDDIRP (504-565)  
TSTPICGQKAL-ITTPLHKETTPKDQKENVGFRPTIIRRSILGTPRTPTPFKNALAAQEKK (509-569)

Fig. 2C

5' untranslated region:

GGCAGCAGAGGAAGTGGCGGCTTTGAGTCCGGTGGCCCAATCGCTGTACTAGTTCTCTGAAGCTCCTCTCGGCTGCTTGC  
CGAGACACCTTGGCGCCAAG

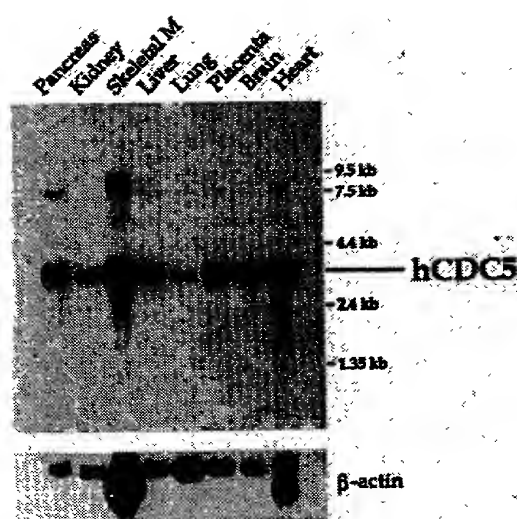
Coding region:

1 DNA BINDING DOMAIN (\_\_\_)  
1 atgcctcgaa ttatgatcaa ggggggccta tggaggaata ccgaggatga aattctgaaa  
61 gcagcggtaa tgaatatag gaaaaatcaa tggcttagga ttgcctcatt gctgcataga  
121 aaatcagcaa agcagtgcga agccagatga tatgaatggc tggatccaag cattaagaag  
181 acagaatggt ccagagaaaga agaggaaaaa ctcttgacat tggccaagtt gatcccaact  
241 cagtgaggga ccattgctcc aatcattgga agaacagcgg ccagtgctt agaacacrat  
301 gaatttcttc tggataaagc tgcccaaaga gacaatgaag aggaacaac agatgatcca  
361 cgaaaactta aacctggaga aatagatcca aatccagaaa caaaaccagc gcggcctgat  
421 ccaattgata tggatgagga tgaacttgag atgctttctg aagccagagc ccgcttggtt  
2 NUCLEAR LOCALIZATION DOMAIN (....)  
481 aatactcagg gaaagaaggc caagaggaaa gcaagagaga aacaattgga agaagcaaga  
541 cgtcttgctg cctccaaaa aagaagagaa ctccgagcag ctggcataga aattcagaag  
601 aaaagaaaaa ggaagagagg agttgattat aatgccgaaa tcccatttga aaaaaagcct  
661 gcccttggtt ttatgatata ttctgaggaa aactaccaag ctcttgacgc agatttcagg  
721 aaattaagac aacaggatct tgatggggag ctaagatctg aaaaagaagg aagagataga  
781 aaaaaagaca aacagcattt gaaaaggaaa aaagaatctg atttaccatc agctattctt  
841 caaactagtg gtgtttctga atttactaaa aagagaagca aactagtact tcctgcccct  
901 cagatttcag atcgagaact ccaggaagtt gtaaaagtag gccaaagcag tgaatttga  
961 cgtcaaaact ccgaggaatc tggcataaca aattctgctt ccagtacact ttgtgtgag  
1021 tacaatgtca ccaacaacag cgttgtctt agaaccacc gaaccaccag tccccaggac  
1081 agaattctgc aggaagccca gaacctcatg gccctcacca atgtggacac cccattgaaa  
3 ACTIVATING DOMAIN (\_\_\_)  
1141 ggtggactta ataccctcatt gcatgagagt gacttctcag gtgtaactcc acagcgacaa  
1201 gttgtacaga ctccaaacac agttctctct actccattca ggactccttc taatggagct  
1261 gaagggctga ctccccggag tggaaacaact cccaaaccag ttattaactc tactccgggt  
1321 agaactcctc ttcgagacaa gttaaacatt aatcccagag atggaatggc agactatagt  
1381 gatccctctt acgtgaagca gatggaaga gaatcccag aacatctccg tttagggttg  
1441 ttgggccttc ctgcccctaa gaatgatttt gaaattgttc taccagaaaa tgccgagaag  
1501 gagctggaag aacgtgaaat agatgatact tacattgaag atgctgctga tgtggatgct  
1561 cgaaagcagg ccatacgaga tgcagagegt gtaaaggaaa tgaaacgaat gcataaagct  
1621 gtccagaaa atctgccaag accatcagaa gtaaatgaaa ctattctaag acccttaaat  
1681 gtagaaccgc ctttaacaga ttacagaaa agtgaagaac taatcaaaaa agaaatgatc  
1741 acaatgcttc attatgacct tctacatcac ccttatgaac catctggaaa taaaaaggc  
1801 aaaactgtag ggtttggtac caataattca gagcacatta cctatctgga acataatcct  
1861 tatgaaaagt tctccaaaga agagctgaaa aaggcccagg atgttttggt gcaggagatg  
1921 gaagtgttta aacaaggaat gagccatgga gagctctcaa gtgaagctta taaccagggtg  
1981 tgggaagaat gctacagtca agttttatat ctccctgggc agagccgcta cacacgggac  
2041 aatctggcta gtaaaaagga cagaattgaa tcacttgaaa agaggctcga gataaacagg  
2101 ggtcacatga cgacagaagc caagagggct gcaaagatgg aaaagaagat gaaaattttg  
2161 cttgggggtt accagtctcg tgctatgggg ctcatgaaac agttgaatga cttatgggac  
2221 caaattgaac aggtcactt ggagttacgc acttttgaag aactcaagaa acatgaagat  
2281 tctgctatc cccggaggct agagtgtcta aaagaagacg ttcagcgaca acaagaaaga  
2341 gaaaaggaac ttcaacatag atatgctgat ttgctgctgg agaaagagac tttaaagtca  
2401 aaattctga

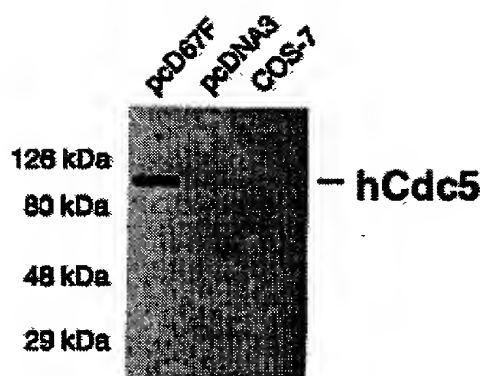
3' untranslated region:

AGTACAGTTATATCTGTGACAGGATTAATTAATGCGGTTTTCATCTCTAGAAGGCTGAAACTG ATGTTTATCTTCATTGACA  
AATTTACCCACCATCTGTGGTTTTCAGTTGTTTAAATGATATCGATCTTACACATCTGTGTATAAAGACCTTAACCTCACA  
GGACGGACATTTTAGAGTTTAAATTATTA AGGCTATCATTCTTTTAGTAATGTCATTTTGCAAACTTTTGTAGTTTGGCCTTTAA  
TTTAAAAAGCCTAATTTTAAAGTGCTGCTGTGAGTAACTCTTGAATAAAACAAATATATAAAA

Fig. 2D

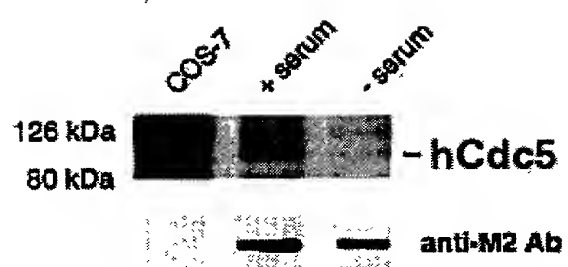


**FIG. 3**



**FIG. 4A**





**FIG. 4B**

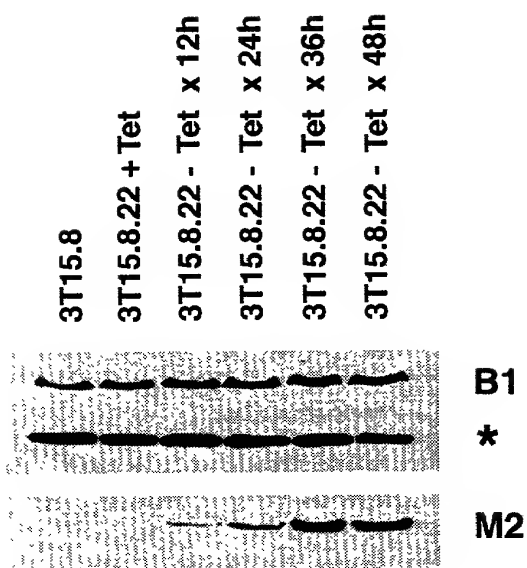
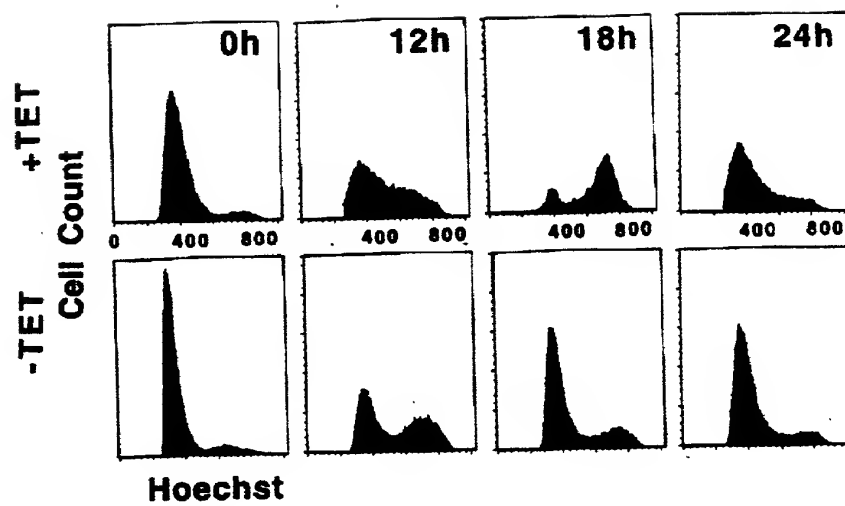


FIG. 5



**Fig. 6**

20250504025260

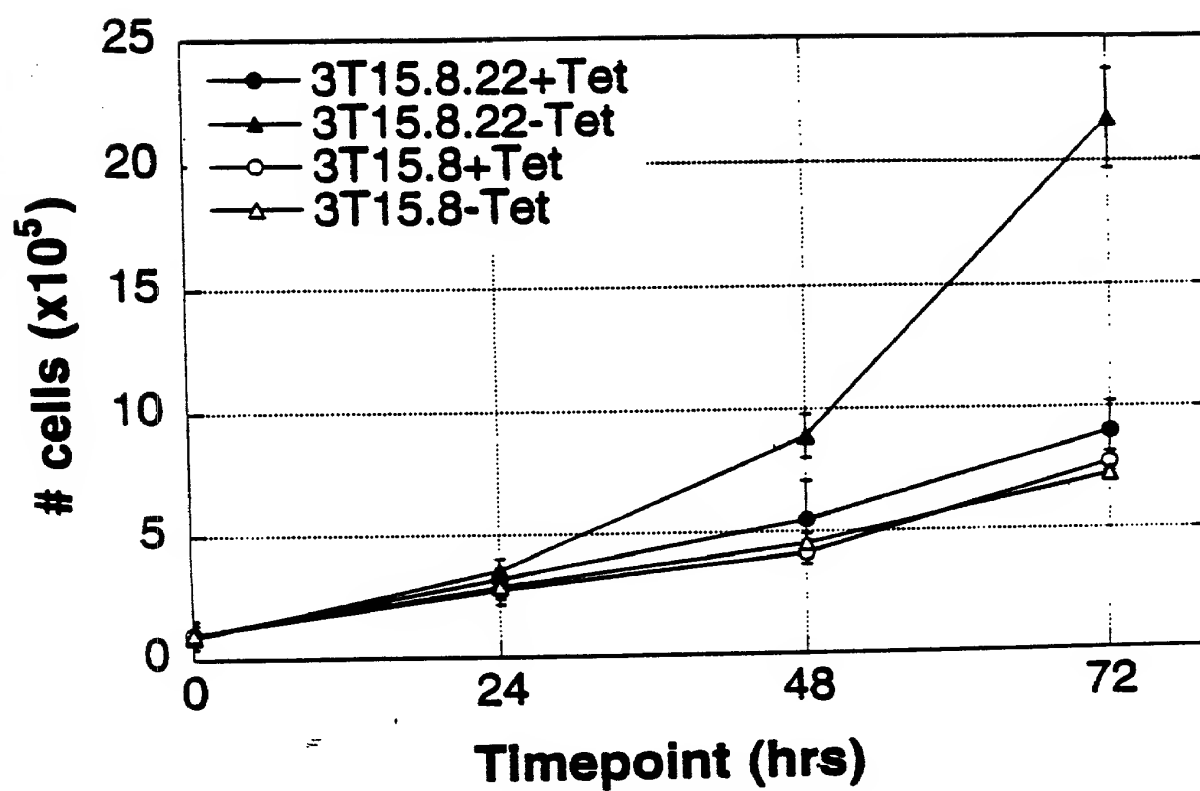
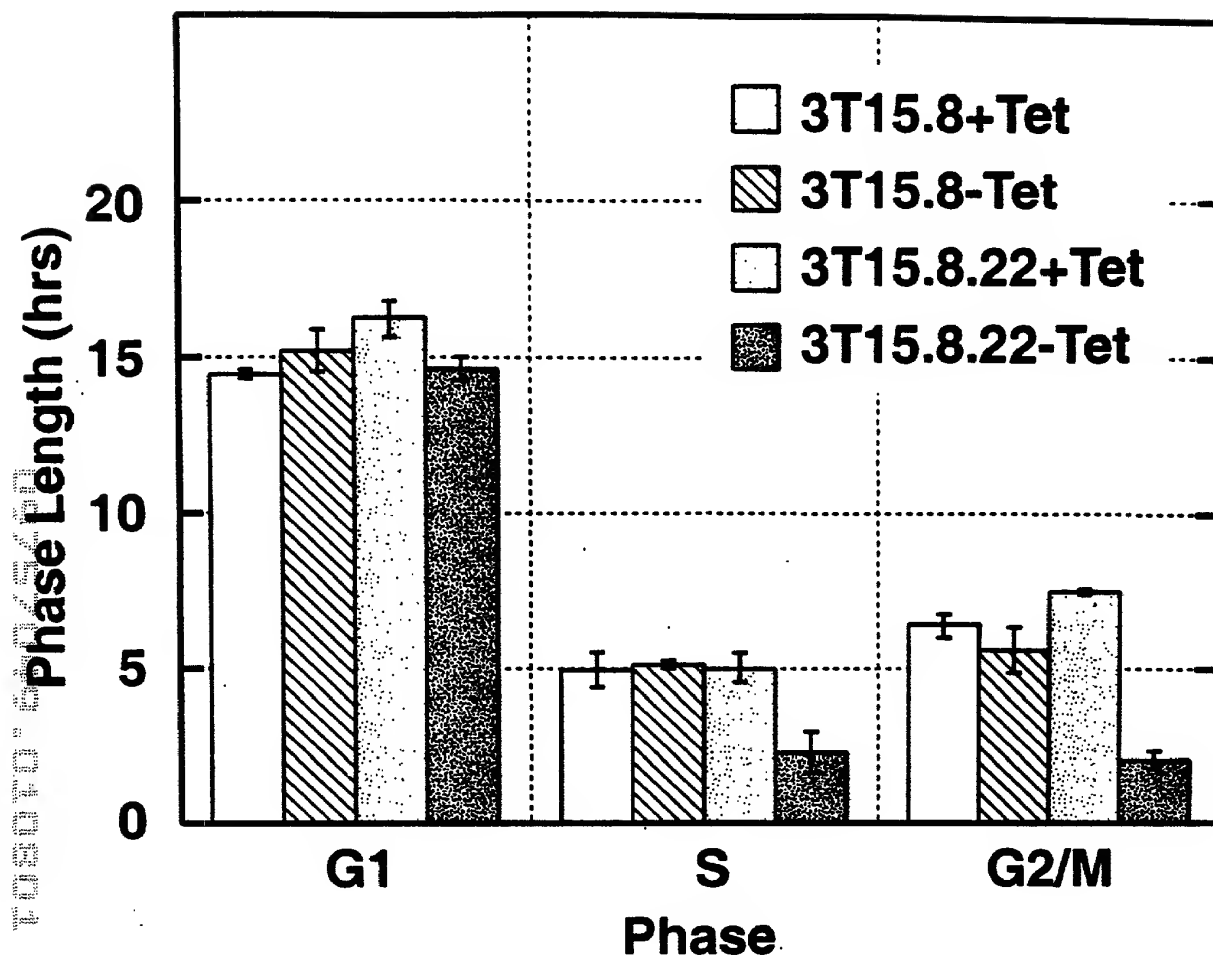


Fig. 7



**FIG. 8**

Downloaded from www.physiology.org at University of California, San Diego on September 11, 2012

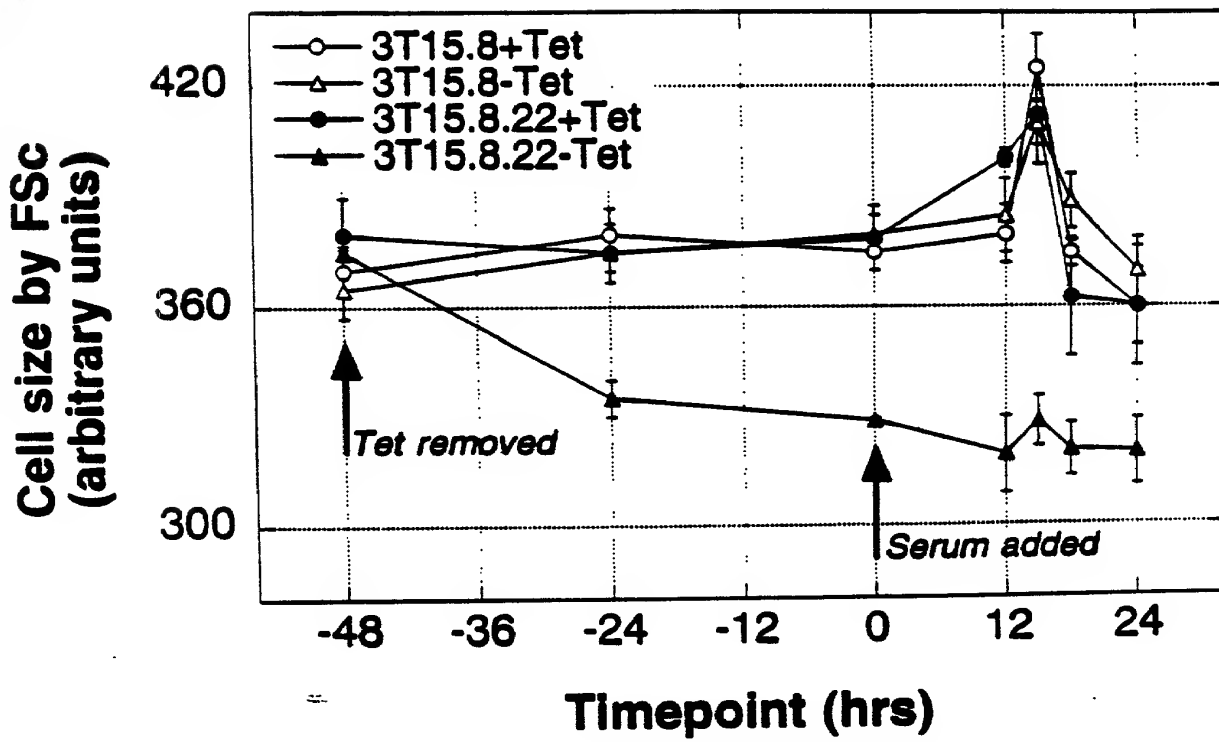


Fig. 9

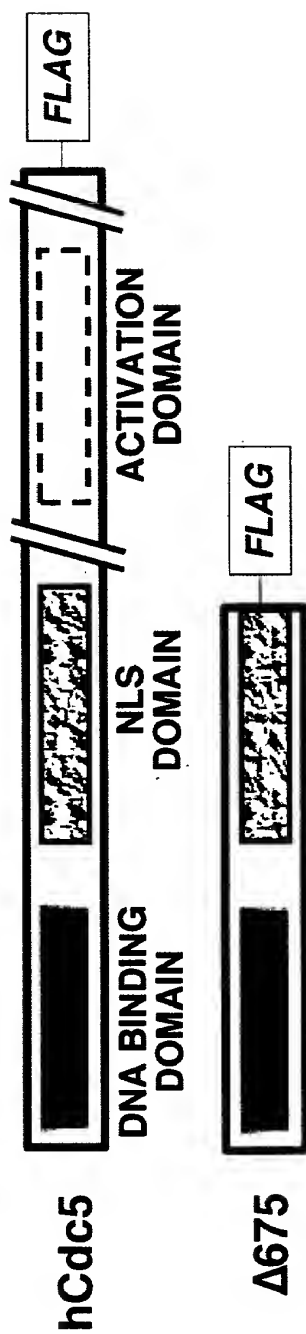


Fig. 10

708070-64029260

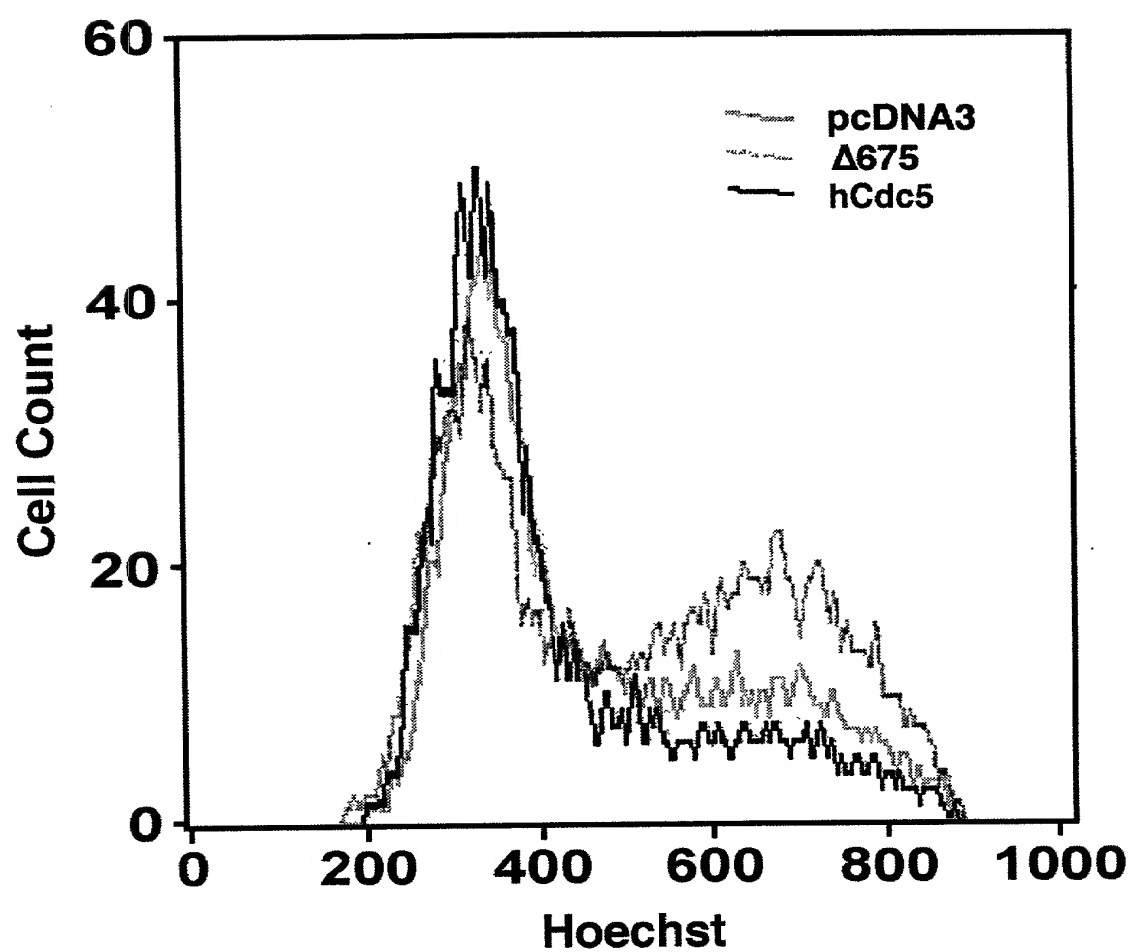
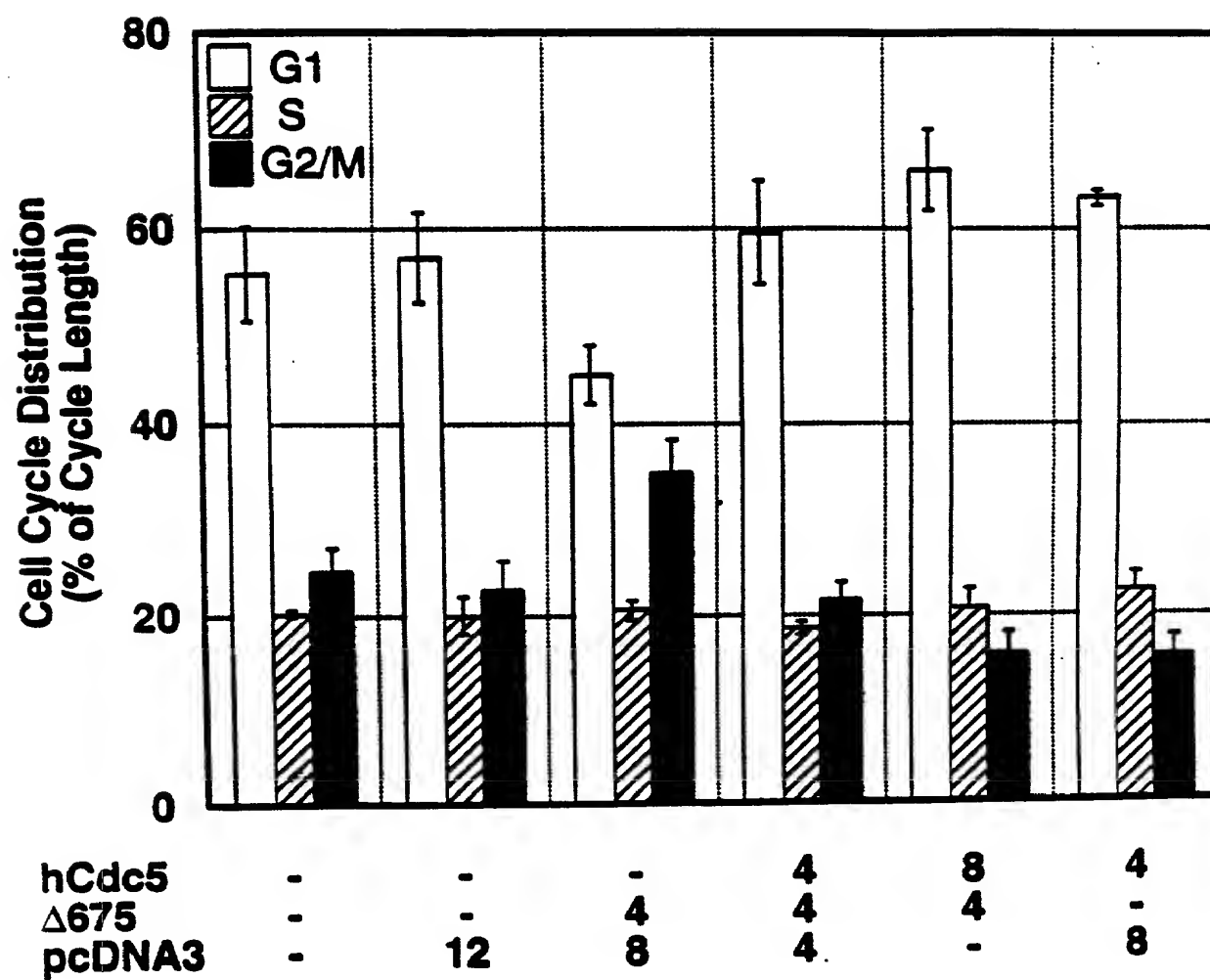


FIG. 11





**Fig. 12**

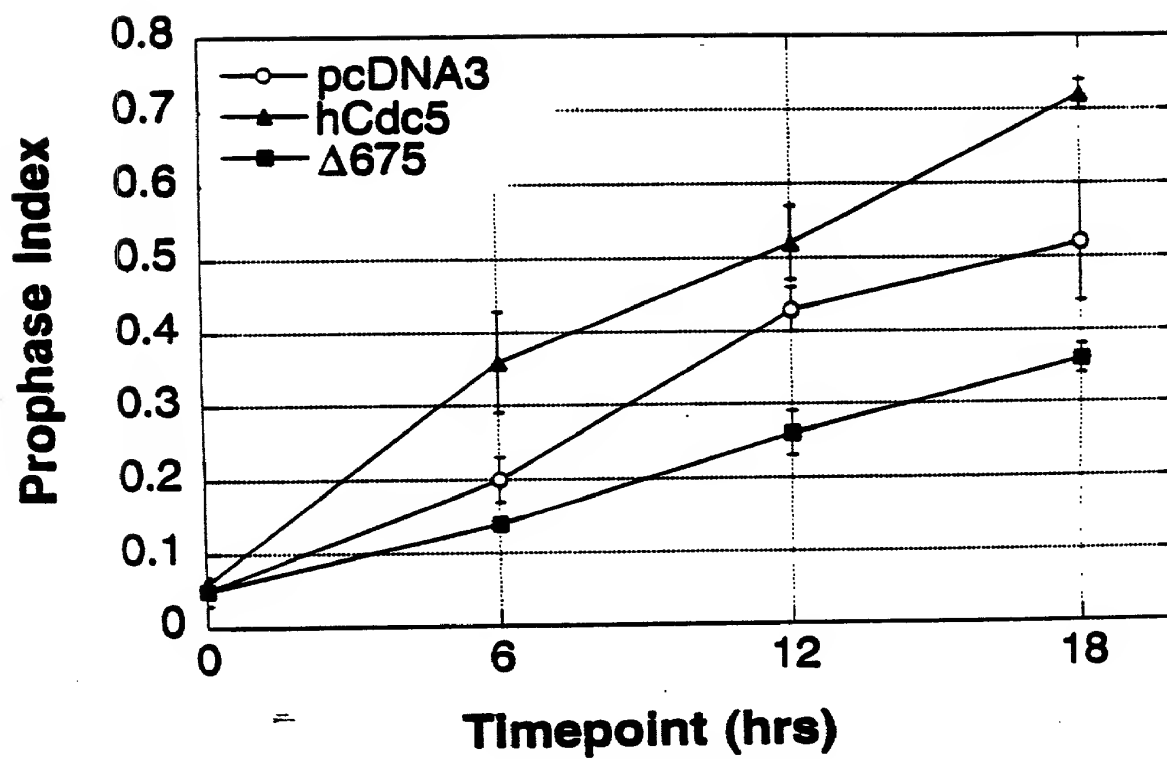
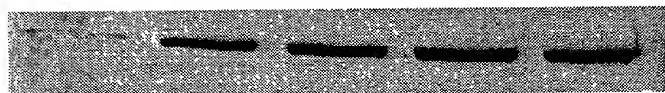


Fig. 13

0 12 15 18 21 hrs



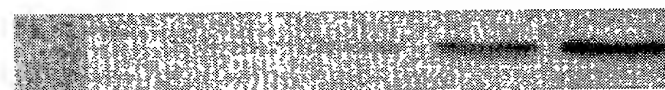
**hCdc5**



**p50 CLNE**

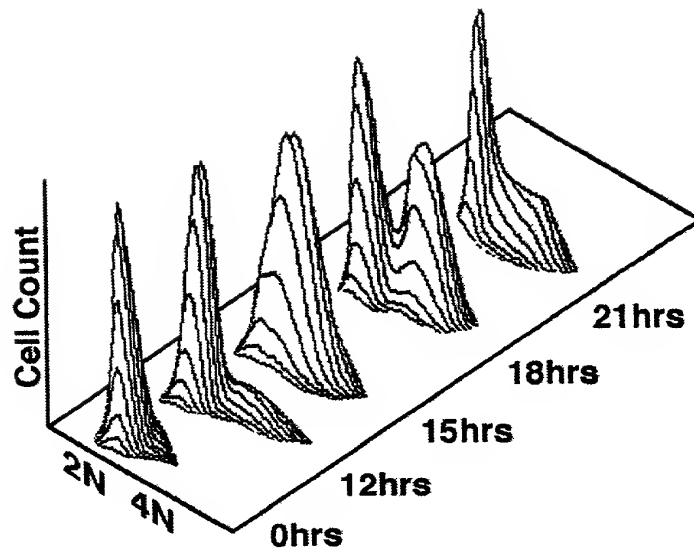


**p60 CLNA**



**p62 CLNB1**

**FIG. 14A**



**FIG. 14B**

Consensus	G A T T T A A C A T A A	(SEQ ID NO:13)
8.05	G A T T T A A C A T A A	
8.04	G A T T T A A C A T A A	
8.03	G A T T T A A C A T A A	
8.02	G A T T T A A C A T A A	
8.01	G A T T T A A C A T A A	
6.05	G G T G T A A C G T G G	(SEQ ID NO:36)
6.04	G T G T T A C C A C A T	(SEQ ID NO:37)
6.03	C C A T A A A T T T A G	(SEQ ID NO:38)
6.02	G A G A T A A A G T C T	(SEQ ID NO:39)
6.01	G T G T T A T T G A A A	(SEQ ID NO:40)
3.05	A C C C A C G T C T A T	(SEQ ID NO:41)
3.04	G G T T A G G A T A G G	(SEQ ID NO:42)
3.03	G T T G A G T A G T A T	(SEQ ID NO:43)
3.02	C T G T T A A T T T C C	(SEQ ID NO:44)
3.01	G G T G T T A T T G A T	(SEQ ID NO:45)

FIG 15